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SEQUENCE LISTING

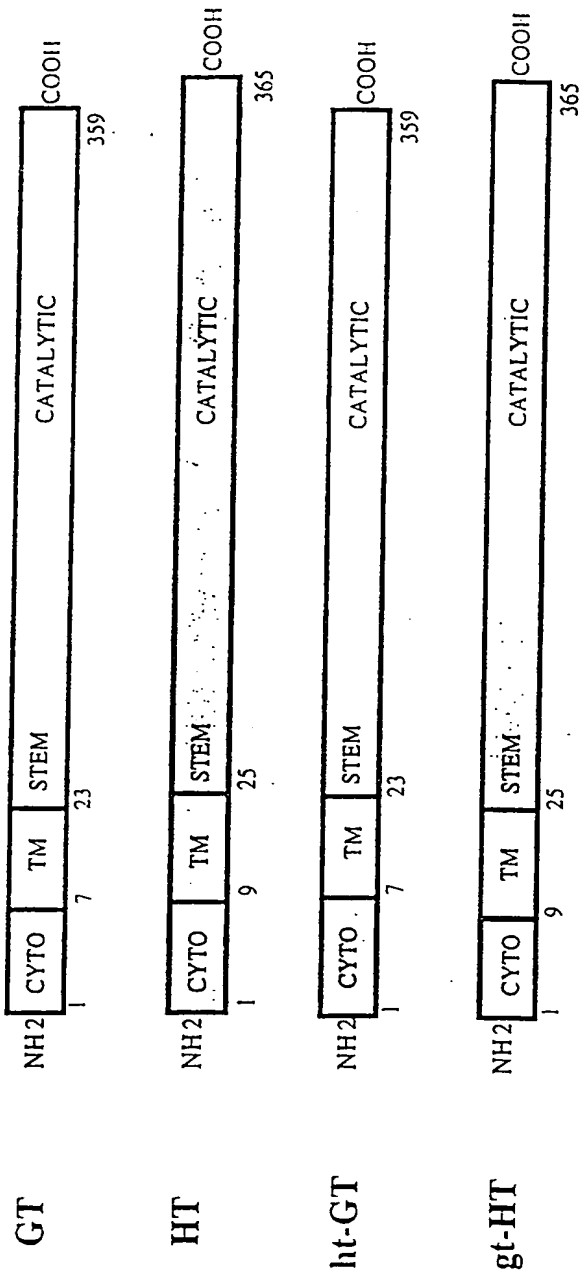


FIGURE 1

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*Sign*

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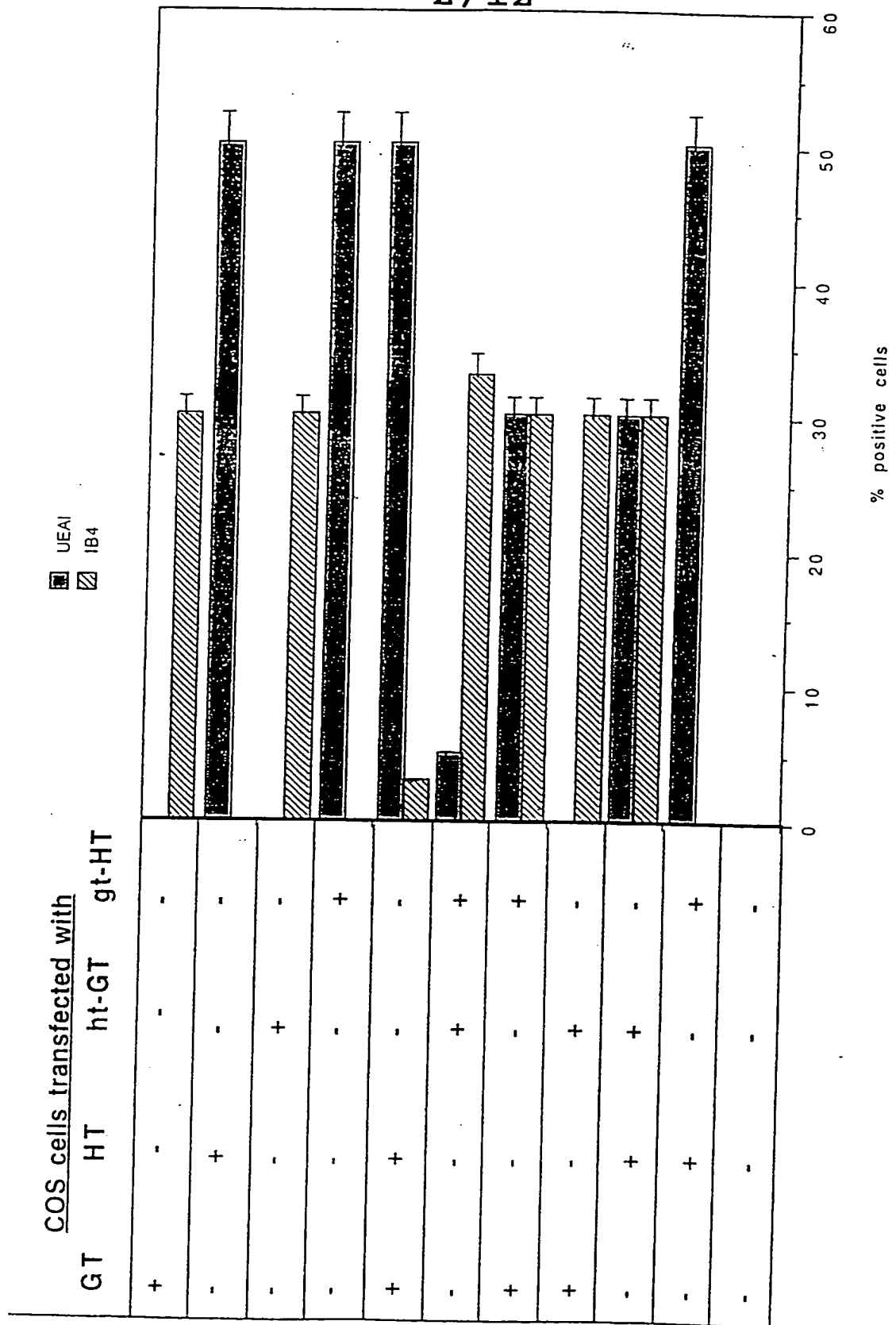


FIGURE 2

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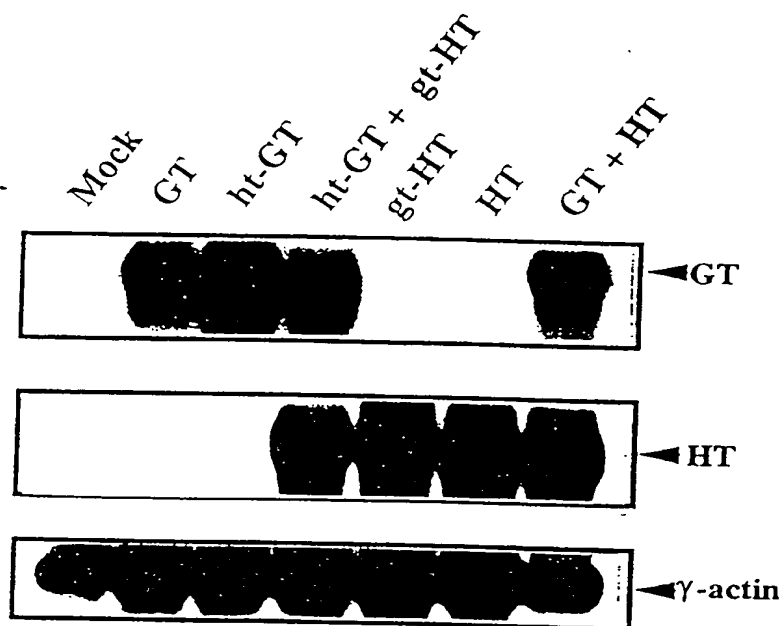


FIGURE 3

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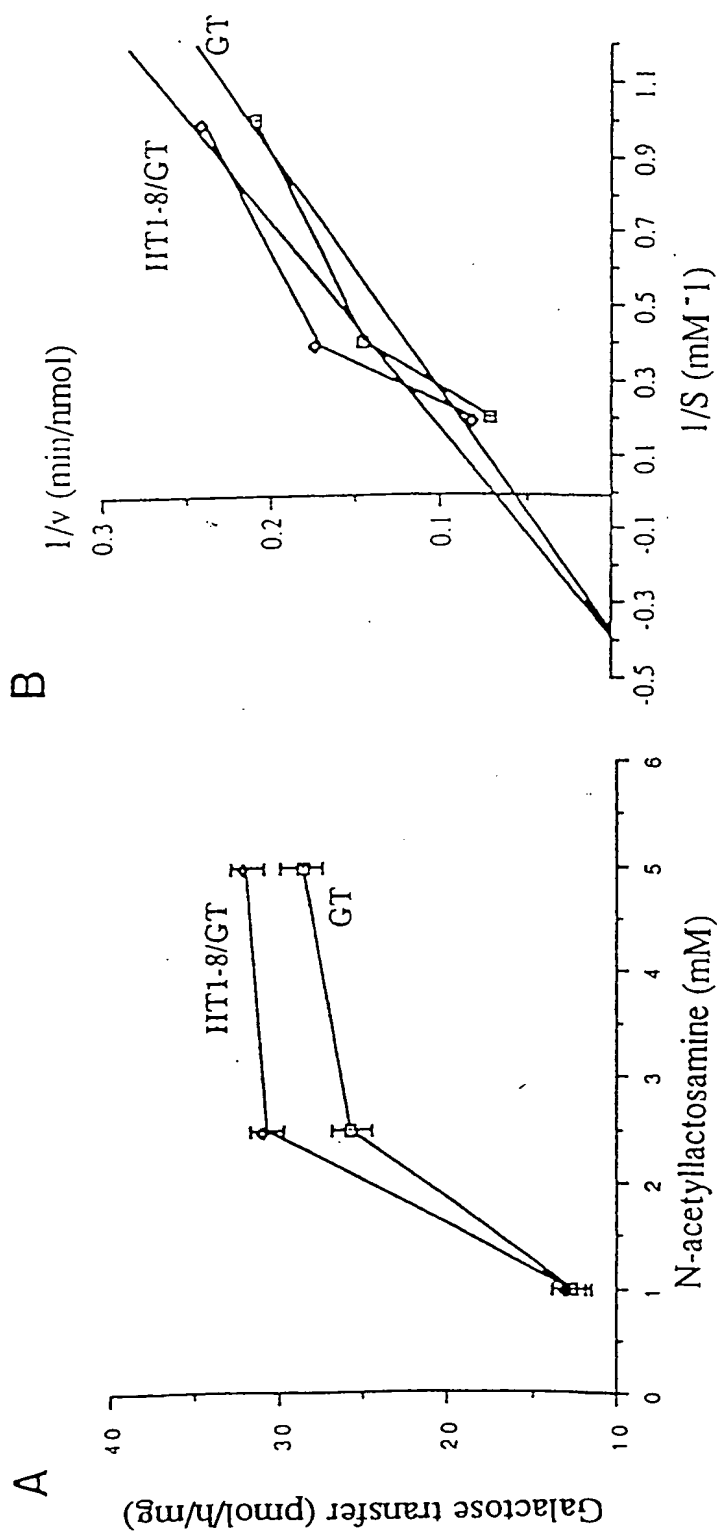


FIGURE 4

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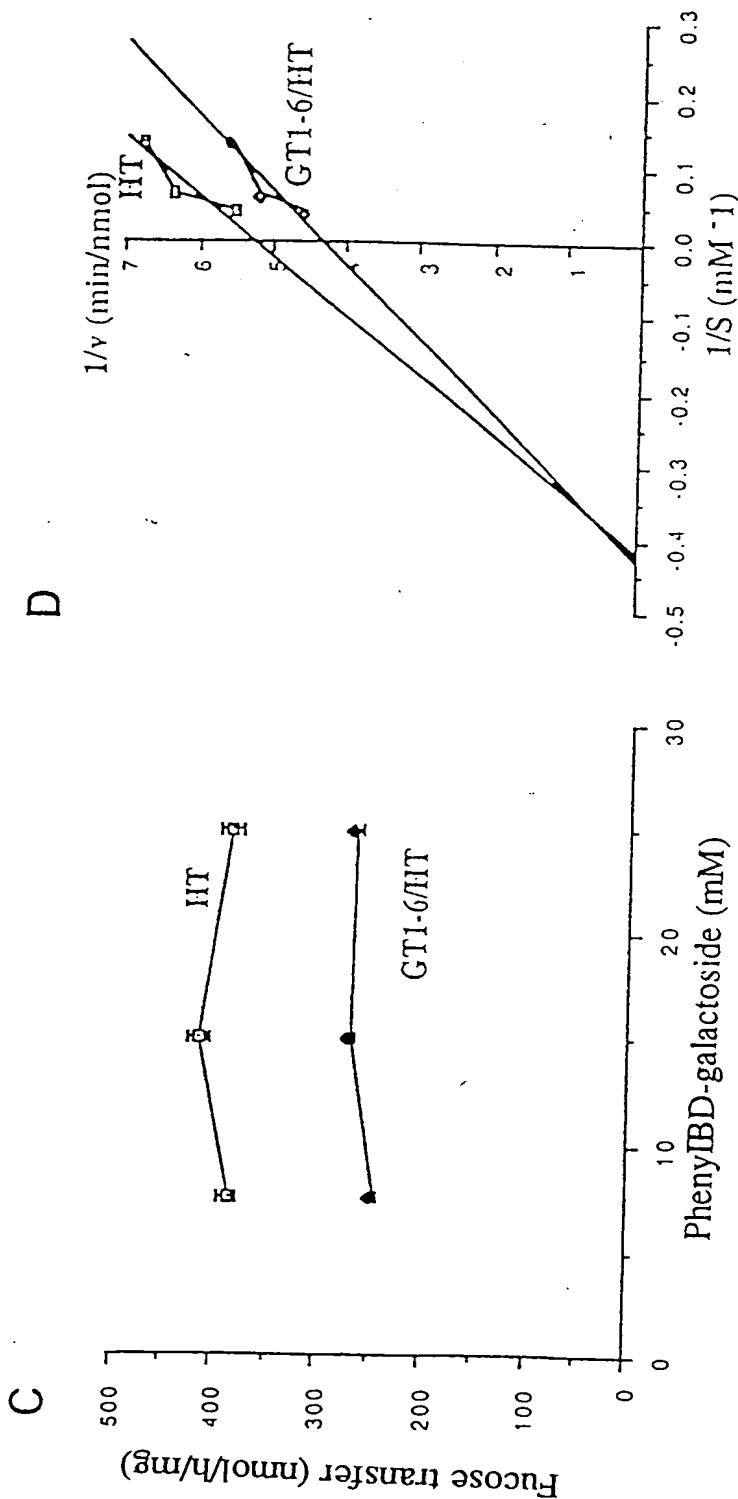


FIGURE 4 Continued

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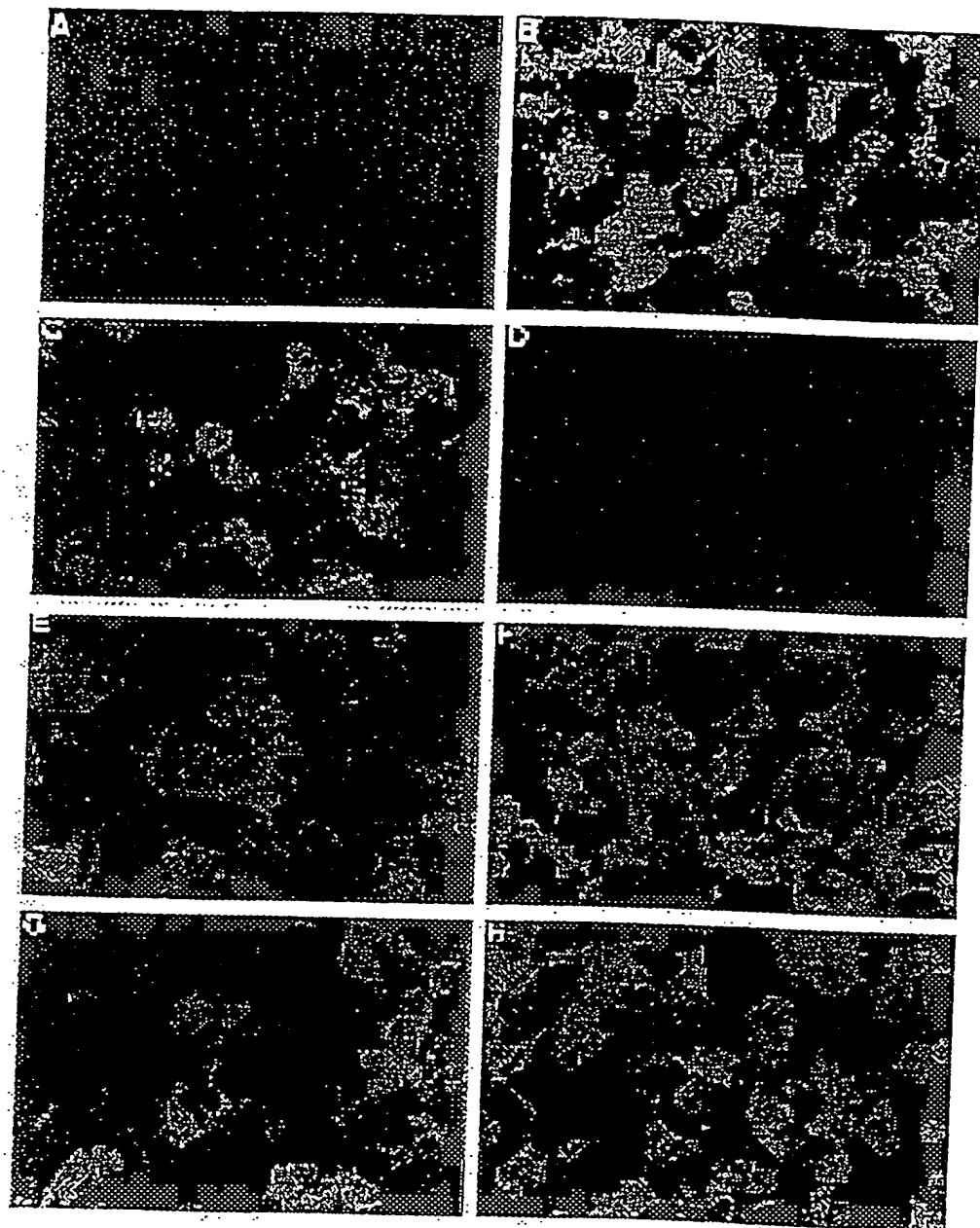


FIGURE 5

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PORCINE SECRETOR SEQUENCE

M L S M Q A S F F P T G P F I L 17  
 CT ACA GCC ATG CTC AGC ATG CAG GCA TCC TTC TTC CCC ACG GGT CCC TTC ATC CTC 59  
 F V F T A S T I F H L Q Q R H V K I Q P 37  
 TTT GTC TTC ACG GCT TCC ACC ATA TTT CAC CAG AGG ATG GTG AAG ATT CAA CCC 119  
 T W E L Q M V T Q V T T E S P S S P Q L 57  
 ACG TGG GAG TTA CAG ATG GTG ACG CAG GTG ACC ACA GAG AGC CCC TCG AGC CCC CAG CTG 179

PORCINE SECRETOR SEQUENCE

K G M W T I N A I G R L G N Q M G E Y A 77  
 AAG GGC ATG TGG ACG ATC AAT GCC ATC GGC CGC CTG GGG AAC CAG ATG GGG GAG TAC GCC 239  
 T L Y A L A R M N G R P A F I P P E M H 97  
 ACC CTG TAC GCG CTG GCC AGG ATG AAC GGC CGG CCG GCC TTC ATC CCG CCC GAG ATG CAC 299  
 S T L A P I F R I T L L P V L H A S T A R 117  
 AGC ACG CTG GCC CCC ATC TTC AGG ATC ACC CTC CCG GTC CTG CAC GCC AGC ACG GCC CGC 359  
 R I P W Q N Y H L N D W M E E R Y R H I 137  
 AGG ATC CCC TGG CAG AAC TAC CAC CTG AAC GAC TGG ATG GAG GAG CGG TAC CGC CAC ATC 419  
 P G E Y V R L T G Y P C S W T F Y H L 157

FIGURE 6

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BATTED "HEOTSDO"

CCG GGG GAG TAC GTG CGC CTC ACG GGC TAC CCC TGC TCC TGG ACC TTC TAC CAC CAC CTG 479  
 R T E I L R E F T L H N H V R E E A Q D 177  
 CGC ACC GAG ATC CTC CGG GAG TTC ACC CTG CAT AAC CAC GTG CGC GAG GAG GCC CAG GAT 539  
 F L R G L R V N G S R P S T Y V G V H V 197  
 TTC CTG CGG GGT CTG CGG GTG AAC GGG AGC CGA CCG AGT ACC TAC GTG GGG GTG CAC GTG 599  
 R R G D Y V H V M P N V W K G V V A D R 217  
 CGC CGG GGG GAC TAC GTG CAC GTG ATG CCC AAC GTG TGG AAG GGC GTG GTG GCC GAC CGG 659  
 R Y L E Q A L D W F R A R Y R S P V F V 237  
 CGG TAC CTG GAG CAG GCC CTG GAC TGG TTC CGG GCT CGC TAC CGC TCC CCC GTC TTT GTG 719  
 V S S N G M A W C R E N I N A S R G D V 257  
 GTC TCC AGC AAC GGC ATG GCC TGG TGT CGG GAA AAC ATC AAT GCC TCG CGC GGC GAT GTG 779  
 V F A G N G I E G S P A K D F A L L T Q 277  
 GTG TTT GCC GGC AAT GGC ATC GAG GGC TCC CCC GCC AAA GAC TTC GCG CTG CTC ACG CAG 839  
 C N H T V M T I G T F G I W A A Y L A G 297  
 TGT AAC CAC ACT GTC ATG ACC ATT GGC ACG TTC GGG ATC TGG GCC TAC CTT GCT GGT 899  
 G E T I Y L A N Y T L P D S P F L K L F 317  
 GGA GAG ACC ATC TAC CTG GCC AAT TAC ACG CTC CCG GAC TCT CCC TTC CTC AAA CTC TTT 959

FIGURE 6 (cont.)

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K P E A A F L P E W I G I E A D L S P L 337  
AAG CCC GAG GCA GCC TTC CTG CCC GAG TGG ATT GGG ATC GAG GCA GAC CTG TCC CCA CTC 1019  
L K H \* 340  
CTT AAG CAC TGA TGT CGG CTG TCC 1043

FIGURE 6 (cont.)

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PIG H TRANSFERASE

M W V P S R R H L C L T F L - L V C V L A 20  
ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTATGCA 60

A I F E L N V Y Q D L F Y S G L D L L A 40  
GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGSCC 120

L C P D H N V V S S P V A I F C L A G T 60  
CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACC 180

P V H P N A S D S C P K H P A S F S G T 80  
CCGSTACACCCCAACGCCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 240

W T I Y P D G R F G N Q M G Q Y A T L L 100  
TGGACTATTTACCCGGATGGCCGGTTTGGGAACAGATGGGACAGTATGCCACGCTGCTG 300

A L A Q L N G R Q A F I Q P A M H A V L 120  
GCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGCTCCTG 360

A P V P R I T L P V L A P E V D R H A P 140  
GCCCCCGTGTTCGCGATCAGGCTGCCTGTCTGCGGCCGAGGCTAGACAGGCACGCTCCT 420

W R E L E L H D W M S E D Y A H L K E P 160  
TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 480

W L K L T G F P C S W T F F H H L R E Q 180  
TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 540

I R S E F T L H D H L R Q E A Q G V L S 200  
ATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGGCCAGGGGGTACTGAGT 600

Q F R L P R T G D R P S T F V G V H V R 220  
CAGTTCGCTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC 660

R G D Y L R V M P K R W K G V V G D G A 240  
CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT 720

Y L Q Q A N D W F R A R Y E A P V F V V 260  
TACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 780

T S N G M E W C R K N I D T S R G D V I 280  
ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 840

F A G D G R E A A P A R D F A L L V Q C 300  
TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 900

N H T I M T I G T F G F W A A Y L A G G 320  
AACCACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGTGGA 960

D T I Y L A N F T L P T S S F L K I F K 340  
GATACCATCTACTTGGCTAAGTTTACCCTGCCCACTTCCAGCTTCTTGAAGATCTTTAAA 1020

P E A A F L P E W V G I N A D L S P L Q 360  
CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG 1080

M L A G P \* 365  
ATGTTGGCTGGGCCTTGA 1093

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FIGURE 7

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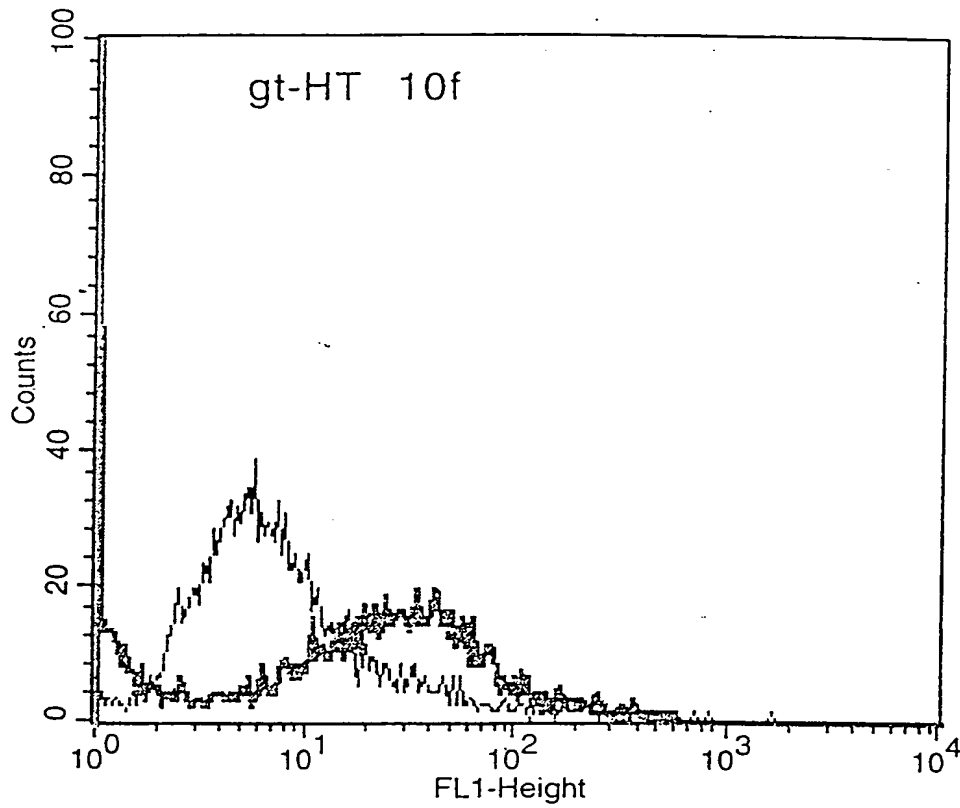


FIGURE 8

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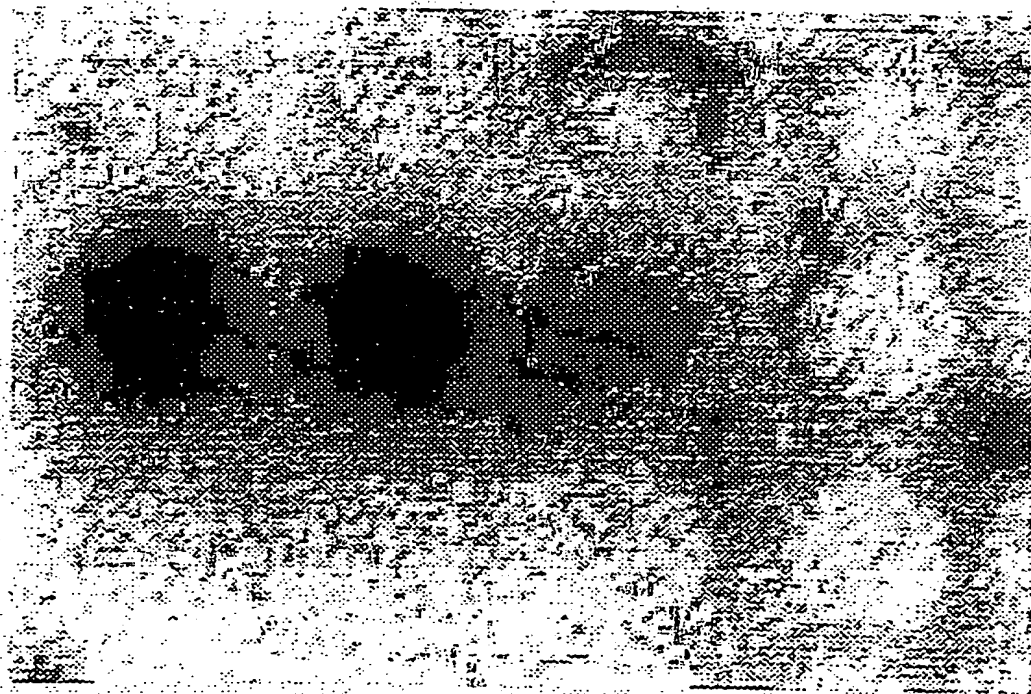


FIGURE 9

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